



PCT10

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,908

DATE: 03/13/2002

TIME: 13:54:43

Input Set : A:\sequence.ST25.txt

Output Set: N:\CRF3\03132002\J069908.raw

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3 <110> APPLICANT: Nielsen, Per Munk
5 <120> TITLE OF INVENTION: Maltogenic Amylase-modified Starch Derivatives
7 <130> FILE REFERENCE: 6001.204-US
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/069,908
C--> 9 <141> CURRENT FILING DATE: 2002-02-28
9 <160> NUMBER OF SEQ ID NOS: 14
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 2160
15 <212> TYPE: DNA
16 <213> ORGANISM: Bacillus sp.
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19 <221> NAME/KEY: CDS
20 <222> LOCATION: (1)..(2157)
21 <223> OTHER INFORMATION:
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25 <221> NAME/KEY: mat_peptide
26 <222> LOCATION: (100)..()
27 <223> OTHER INFORMATION:
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33          -30          -25          -20
35 ggt ctt ctg ttc agc ggt tct ctt ccg tac aat cca aac gcc gct gaa      96
36 Gly Leu Leu Phe Ser Gly Ser Leu Pro Tyr Asn Pro Asn Ala Ala Glu
37          -15          -10          -5
39 gcc agc agt tcc gca agc gtc aaa ggg gac gtg att tac cag att atc      144
40 Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
41 -1 1          5          10          15
43 att gac cgg ttt tac gat ggg gac acg acg aac aac aat cct gcc aaa      192
44 Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
45          20          25          30
47 agt tat gga ctt tac gat ccg acc aaa tcg aag tgg aaa atg tat tgg      240
48 Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
49          35          40          45
51 ggc ggg gat ctg gag ggg gtt cgt caa aaa ctt cct tat ctt aaa cag      288
52 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
53          50          55          60
55 ctg ggc gta acg aca atc tgg ttg tcc ccg gtt ttg gac aat ctg gat      336
56 Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
57          65          70          75
59 aca ctg gcg ggc acc gat aac acg ggc tat cac gga tac tgg acg cgc      384
60 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg

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61	80					85						90				95	
63	gat	ttt	aaa	cag	att	gag	gaa	cat	ttc	ggg	aat	tgg	acc	aca	ttt	gac	432
64	Asp	Phe	Lys	Gln	Ile	Glu	Glu	His	Phe	Gly	Asn	Trp	Thr	Thr	Phe	Asp	
65						100				105					110		
67	acg	ttg	gtc	aat	gat	gct	cac	caa	aac	gga	atc	aag	gtg	att	gtc	gac	480
68	Thr	Leu	Val	Asn	Asp	Ala	His	Gln	Asn	Gly	Ile	Lys	Val	Ile	Val	Asp	
69				115					120					125			
71	ttt	gtg	ccc	aat	cat	tcg	act	cct	ttt	aag	gca	aac	gat	tcc	acc	ttt	528
72	Phe	Val	Pro	Asn	His	Ser	Thr	Pro	Phe	Lys	Ala	Asn	Asp	Ser	Thr	Phe	
73			130					135					140				
75	gcg	gaa	ggc	ggc	gcc	ctc	tac	aac	aat	gga	acc	tat	atg	ggc	aat	tat	576
76	Ala	Glu	Gly	Gly	Ala	Leu	Tyr	Asn	Asn	Gly	Thr	Tyr	Met	Gly	Asn	Tyr	
77		145				150				155							
79	ttt	gat	gac	gca	aca	aaa	ggg	tac	ttc	cac	cat	aat	ggg	gac	atc	agc	624
80	Phe	Asp	Asp	Ala	Thr	Lys	Gly	Tyr	Phe	His	His	Asn	Gly	Asp	Ile	Ser	
81	160					165				170				175			
83	aac	tgg	gac	gac	cgg	tac	gag	gcg	caa	tgg	aaa	aac	ttc	acg	gat	cca	672
84	Asn	Trp	Asp	Asp	Arg	Tyr	Glu	Ala	Gln	Trp	Lys	Asn	Phe	Thr	Asp	Pro	
85				180					185					190			
87	gcc	ggt	ttc	tcg	ctt	gcc	gat	ttg	tcg	cag	gaa	aat	ggc	acg	att	gct	720
88	Ala	Gly	Phe	Ser	Leu	Ala	Asp	Leu	Ser	Gln	Glu	Asn	Gly	Thr	Ile	Ala	
89			195					200					205				
91	caa	tac	ctg	acc	gat	gcg	gcg	gtt	caa	ttg	gta	gca	cat	gga	gcg	gat	768
92	Gln	Tyr	Leu	Thr	Asp	Ala	Ala	Val	Gln	Leu	Val	Ala	His	Gly	Ala	Asp	
93		210				215				220							
95	ggt	ttg	cgg	att	gat	gcg	gtg	aag	cat	ttt	aat	tcg	ggg	ttc	tcc	aaa	816
96	Gly	Leu	Arg	Ile	Asp	Ala	Val	Lys	His	Phe	Asn	Ser	Gly	Phe	Ser	Lys	
97		225				230				235							
99	tcg	ttg	gcc	gat	aaa	ctg	tac	caa	aag	aaa	gac	att	ttc	ctg	gtg	ggg	864
100	Ser	Leu	Ala	Asp	Lys	Leu	Tyr	Gln	Lys	Lys	Asp	Ile	Phe	Leu	Val	Gly	
101	240					245				250				255			
103	gaa	tgg	tac	gga	gat	gac	ccc	gga	aca	gcc	aat	cat	ctg	gaa	aag	gtc	912
104	Glu	Trp	Tyr	Gly	Asp	Asp	Pro	Gly	Thr	Ala	Asn	His	Leu	Glu	Lys	Val	
105				260				265					270				
107	cgg	tac	gcc	aac	aac	agc	ggt	gtc	aat	gtg	ctg	gat	ttt	gat	ctc	aac	960
108	Arg	Tyr	Ala	Asn	Asn	Ser	Gly	Val	Asn	Val	Leu	Asp	Phe	Asp	Leu	Asn	
109			275					280					285				
111	acg	gtg	att	cga	aat	gtg	ttc	ggc	aca	ttt	acg	caa	acg	atg	tac	gat	1008
112	Thr	Val	Ile	Arg	Asn	Val	Phe	Gly	Thr	Phe	Thr	Gln	Thr	Met	Tyr	Asp	
113			290					295					300				
115	ctt	aac	aat	atg	gtg	aac	caa	acg	ggg	aac	gag	tac	aaa	tac	aaa	gaa	1056
116	Leu	Asn	Asn	Met	Val	Asn	Gln	Thr	Gly	Asn	Glu	Tyr	Lys	Tyr	Lys	Glu	
117		305				310				315							
119	aat	cta	atc	aca	ttt	atc	gat	aac	cat	gat	atg	tca	aga	ttt	ctt	tcg	1104
120	Asn	Leu	Ile	Thr	Phe	Ile	Asp	Asn	His	Asp	Met	Ser	Arg	Phe	Leu	Ser	
121	320					325				330				335			
123	gta	aat	tcg	aac	aag	gcg	aat	ttg	cac	cag	gcg	ctt	gct	ttc	att	ctc	1152
124	Val	Asn	Ser	Asn	Lys	Ala	Asn	Leu	His	Gln	Ala	Leu	Ala	Phe	Ile	Leu	
125				340				345					350				

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127	act	tcg	cgg	ggt	acg	ccc	tcc	atc	tat	tat	gga	acc	gaa	caa	tac	atg	1200
128	Thr	Ser	Arg	Gly	Thr	Pro	Ser	Ile	Tyr	Tyr	Gly	Thr	Glu	Gln	Tyr	Met	
129				355					360					365			
131	gca	ggc	ggc	aat	gac	ccg	tac	aac	cgg	ggg	atg	atg	ccg	gcg	ttt	gat	1248
132	Ala	Gly	Gly	Asn	Asp	Pro	Tyr	Asn	Arg	Gly	Met	Met	Pro	Ala	Phe	Asp	
133				370				375					380				
135	acg	aca	acc	acc	gcc	ttt	aaa	gag	gtg	tca	act	ctg	gcg	ggg	ttg	cgc	1296
136	Thr	Thr	Thr	Thr	Ala	Phe	Lys	Glu	Val	Ser	Thr	Leu	Ala	Gly	Leu	Arg	
137		385					390					395					
139	agg	aac	aat	gcg	gcg	atc	cag	tac	ggc	acc	acc	acc	cag	cgt	tgg	atc	1344
140	Arg	Asn	Asn	Ala	Ala	Ile	Gln	Tyr	Gly	Thr	Thr	Thr	Gln	Arg	Trp	Ile	
141	400					405					410				415		
143	aac	aat	gat	gtt	tac	att	tat	gaa	cgg	aaa	ttt	ttc	aac	gat	gtc	gtg	1392
144	Asn	Asn	Asp	Val	Tyr	Ile	Tyr	Glu	Arg	Lys	Phe	Phe	Asn	Asp	Val	Val	
145				420				425					430				
147	ttg	gtg	gcc	atc	aat	cga	aac	acg	caa	tcc	tcc	tat	tcg	att	tcc	ggt	1440
148	Leu	Val	Ala	Ile	Asn	Arg	Asn	Thr	Gln	Ser	Ser	Tyr	Ser	Ile	Ser	Gly	
149				435				440					445				
151	ttg	cag	acg	gcc	ttg	cca	aat	ggc	agc	tat	gcg	gat	tat	ctg	tca	ggg	1488
152	Leu	Gln	Thr	Ala	Leu	Pro	Asn	Gly	Ser	Tyr	Ala	Asp	Tyr	Leu	Ser	Gly	
153				450				455					460				
155	ctg	ttg	ggg	ggg	aac	ggg	att	tcc	gtt	tcc	aat	gga	agt	gtc	gct	tcg	1536
156	Leu	Leu	Gly	Gly	Asn	Gly	Ile	Ser	Val	Ser	Asn	Gly	Ser	Val	Ala	Ser	
157		465					470					475					
159	ttc	acg	ctt	gcg	cct	gga	gcc	gtg	tct	gtt	tgg	cag	tac	agc	aca	tcc	1584
160	Phe	Thr	Leu	Ala	Pro	Gly	Ala	Val	Ser	Val	Trp	Gln	Tyr	Ser	Thr	Ser	
161	480					485				490					495		
163	gct	tca	gcg	ccg	caa	atc	gga	tcg	gtt	gct	cca	aat	atg	ggg	att	ccg	1632
164	Ala	Ser	Ala	Pro	Gln	Ile	Gly	Ser	Val	Ala	Pro	Asn	Met	Gly	Ile	Pro	
165				500				505						510			
167	ggt	aat	gtg	gtc	acg	atc	gac	ggg	aaa	ggt	ttt	ggg	acg	acg	cag	gga	1680
168	Gly	Asn	Val	Val	Thr	Ile	Asp	Gly	Lys	Gly	Phe	Gly	Thr	Thr	Gln	Gly	
169				515				520					525				
171	acc	gtg	aca	ttt	ggc	gga	gtg	aca	gcg	act	gtg	aaa	tcc	tgg	aca	tcc	1728
172	Thr	Val	Thr	Phe	Gly	Gly	Val	Thr	Ala	Thr	Val	Lys	Ser	Trp	Thr	Ser	
173				530				535					540				
175	aat	cgg	att	gaa	gtg	tac	gtt	ccc	aac	atg	gcc	gcc	ggg	ctg	acc	gat	1776
176	Asn	Arg	Ile	Glu	Val	Tyr	Val	Pro	Asn	Met	Ala	Ala	Gly	Leu	Thr	Asp	
177		545					550					555					
179	gtg	aaa	gtc	acc	gcg	ggt	gga	gtt	tcc	agc	aat	ctg	tat	tct	tac	aat	1824
180	Val	Lys	Val	Thr	Ala	Gly	Gly	Val	Ser	Ser	Asn	Leu	Tyr	Ser	Tyr	Asn	
181	560					565				570					575		
183	att	ttg	agt	gga	acg	cag	aca	tcg	gtt	gtg	ttt	act	gtg	aaa	agt	gcg	1872
184	Ile	Leu	Ser	Gly	Thr	Gln	Thr	Ser	Val	Val	Phe	Thr	Val	Lys	Ser	Ala	
185				580				585					590				
187	cct	ccg	acc	aac	ctg	ggg	gat	aag	att	tac	ctg	acg	ggc	aac	ata	ccg	1920
188	Pro	Pro	Thr	Asn	Leu	Gly	Asp	Lys	Ile	Tyr	Leu	Thr	Gly	Asn	Ile	Pro	
189				595				600					605				
191	gaa	ttg	ggg	aat	tgg	agc	acg	gat	acg	agc	gga	gcc	gtt	aac	aat	gcg	1968

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192 Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
193      610      615      620
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196 Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
197      625      630      635
199 agc gtt cca gca gga aag acg att caa ttc aag ttc ttc atc aag cgt      2064
200 Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
201 640      645      650      655
203 gcg gat gga acg att caa tgg gag aat ggt tcg aac cac gtg gcc aca      2112
204 Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr
205      660      665      670
207 act ccc acg ggt gca acc ggt aac att act gtt acg tgg caa aac tag      2160
208 Thr Pro Thr Gly Ala Thr Gly Asn Ile Thr Val Thr Trp Gln Asn
209      675      680      685
212 <210> SEQ ID NO: 2
213 <211> LENGTH: 719
214 <212> TYPE: PRT
215 <213> ORGANISM: Bacillus sp.
217 <400> SEQUENCE: 2
219 Met Lys Lys Lys Thr Leu Ser Leu Phe Val Gly Leu Met Leu Leu Ile
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223 Gly Leu Leu Phe Ser Gly Ser Leu Pro Tyr Asn Pro Asn Ala Ala Glu
224      -15      -10      -5
227 Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
228 -1 1      5      10      15
231 Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
232      20      25      30
235 Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
236      35      40      45
239 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
240      50      55      60
243 Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
244      65      70      75
247 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
248 80      85      90      95
251 Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
252      100      105      110
255 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
256      115      120      125
259 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
260      130      135      140
263 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
264      145      150      155
267 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
268 160      165      170      175
271 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
272      180      185      190
275 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
276      195      200      205

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279 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
280      210      215      220
283 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
284      225      230      235
287 Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
288 240      245      250      255
291 Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
292      260      265      270
295 Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn
296      275      280      285
299 Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
300      290      295      300
303 Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
304      305      310      315
307 Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
308 320      325      330      335
311 Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
312      340      345      350
315 Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met
316      355      360      365
319 Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp
320      370      375      380
323 Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg
324      385      390      395
327 Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile
328 400      405      410      415
331 Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val
332      420      425      430
335 Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly
336      435      440      445
339 Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly
340      450      455      460
343 Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser
344      465      470      475
347 Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser
348 480      485      490      495
351 Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro
352      500      505      510
355 Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly
356      515      520      525
359 Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser
360      530      535      540
363 Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp
364      545      550      555
367 Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn
368 560      565      570      575
371 Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala
372      580      585      590
375 Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date